

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Shah, Purvi
Corley, Neil C.

(ii) TITLE OF THE INVENTION: HUMAN PEROXISOMAL THIOESTERASE

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0293 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRAINOT09
(B) CLONE: 2150905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Gly	Arg	Ala	Val	Ala	Thr	Ala	Ala	Leu	Pro	Pro	Gly	Asp	Leu	Arg
1				5					10					15	
Ser	Val	Leu	Val	Thr	Thr	Val	Leu	Asn	Leu	Glu	Pro	Leu	Asp	Glu	Asp
			20					25					30		
Leu	Phe	Arg	Gly	Arg	His	Tyr	Trp	Val	Pro	Ala	Lys	Arg	Leu	Phe	Gly
	35						40					45			

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Gly Gln Ile Val Gly Gln Ala Leu Val Ala Ala Ala Lys Ser Val Ser
 50 55 60
 Glu Asp Val His Val His Ser Leu His Cys Tyr Phe Val Arg Ala Gly
 65 70 75 80
 Asp Pro Lys Leu Pro Val Leu Tyr Gln Val Glu Arg Thr Arg Thr Gly
 85 90 95
 Ser Ser Phe Ser Val Arg Ser Val Lys Ala Val Gln His Gly Lys Pro
 100 105 110
 Ile Phe Ile Cys Gln Ala Ser Phe Gln Gln Ala Gln Pro Ser Pro Met
 115 120 125
 Gln His Gln Phe Ser Met Pro Thr Val Pro Pro Pro Glu Glu Leu Leu
 130 135 140
 Asp Cys Glu Thr Leu Ile Asp Gln Tyr Leu Arg Asp Pro Asn Leu Gln
 145 150 155 160
 Lys Arg Tyr Pro Leu Ala Leu Asn Arg Ile Ala Ala Gln Glu Val Pro
 165 170 175
 Ile Glu Ile Lys Pro Val Asn Pro Ser Pro Leu Ser Gln Leu Gln Arg
 180 185 190
 Met Glu Pro Lys Gln Met Phe Trp Val Arg Ala Arg Gly Tyr Ile Gly
 195 200 205
 Glu Gly Asp Met Lys Met His Cys Cys Val Ala Ala Tyr Ile Ser Asp
 210 215 220
 Tyr Ala Phe Leu Gly Thr Ala Leu Leu Pro His Gln Trp Gln His Lys
 225 230 235 240
 Val His Phe Met Val Ser Leu Asp His Ser Met Trp Phe His Ala Pro
 245 250 255
 Phe Arg Ala Asp His Trp Met Leu Tyr Glu Cys Glu Ser Pro Trp Ala
 260 265 270
 Gly Gly Ser Arg Gly Leu Val His Gly Arg Leu Trp Arg Gln Asp Gly
 275 280 285
 Val Leu Ala Val Thr Cys Ala Gln Glu Gly Val Ile Arg Val Lys Pro
 290 295 300
 Gln Val Ser Glu Ser Lys Leu
 305 310

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAINOT09
 (B) CLONE: 2150905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCATTGAA	CTAGATGTCG	TCCCCGCAGG	CCCCAGAAGA	TGGGCAGGGC	TGTGGCGACC	60
GCGGCGCTTC	CCCCTGGGGA	CCTCCGTAGC	GTCTTGGTCA	CGACCGTGCT	CAACCTCGAG	120
CCGCTGGACG	AGGATCTCTT	CAGAGGAAGG	CATTACTGGG	TACCGGCCAA	GAGGCTGTTT	180
GGTGGTCAGA	TCGTGGGCCA	GGCCCTGGTG	GCTGCAGCCA	AGTCTGTGAG	TGAAGACGTC	240
CACGTGCACT	CCCTGCACTG	CTACTTTGTT	CGGGCAGGGG	ACCCGAAGCT	GCCAGTACTG	300
TACCAAGTGG	AGCGGACACG	AACAGGGTCG	AGCTTCTCGG	TGCGCTCTGT	GAAGGCCGTG	360
CAACATGGGA	AGCCCATCTT	CATCTGCCAG	GCCTCCTTCC	AGCAGGCCCA	GCCCAGCCCC	420
ATGCAGCACC	AGTTCTCCAT	GCCCACTGTG	CCACCACCAG	AAGAGCTGCT	TGACTGTGAG	480
ACCCTCATTG	ACCAATTTT	AAGGGACCTT	AACCTCCAAA	AGAGGTACCC	ATTGGCGCTC	540
AACCGAATTG	CTGCTCAGGA	GGTCCCCATT	GAGATCAAGC	CAGTAAACCC	ATCCCCCCTG	600
AGCCAGCTGC	AGAGAATGGA	GCCCAAACAG	ATGTTCTGGG	TGCGAGCCCC	GGGCTATATT	660
GGCGAGGGCG	ACATGAAGAT	GCACTGCTGC	GTGGCCGCCT	ATATCTCCGA	CTATGCCTTC	720
TTGGGCACTG	CACTGCTGCC	TCACCAGTGG	CAGCACAAGG	TGCACTTCAT	GGTCTCACTG	780
GACCATTTCA	TGTGGTTCCA	CGCCCCCTTC	CGAGCTGACC	ACTGGATGCT	CTATGAATGC	840
GAGAGCCCCCT	GGGCCGGTGG	CTCTCGGGGG	CTGGTCCATG	GGCGGCTGTG	GCGTCAGGAT	900
GGAGTCCTAG	CTGTGACCTG	TGCCCAGGAG	GGCGTGATCC	GAGTGAAGCC	CCAGGTCTCA	960
GAGAGCAAGC	TGTAGCCAGA	GGTACCAGCT	TCGCCTGGGG	CTTCAAGAAC	CTCCCATCTA	1020

TCCCCATTCC TGAGACAGGA GTTACAGTCC CTTTGGCCCC TCACATCCAA TAAAGAGACT
GATACCACTG GAAAAAAA

1080
1098

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 147932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Gln Ala Leu Lys Asn Leu Leu Thr Leu Leu Asn Leu Glu Lys
1 5 10 15
Ile Glu Glu Gly Leu Phe Arg Gly Gln Ser Glu Asp Leu Gly Leu Arg
20 25 30
Gln Val Phe Gly Gly Gln Val Val Gly Gln Ala Leu Tyr Ala Ala Lys
35 40 45
Glu Thr Val Pro Glu Glu Arg Leu Val His Ser Phe His Ser Tyr Phe
50 55 60
Leu Arg Pro Gly Asp Ser Lys Lys Pro Ile Ile Tyr Asp Val Glu Thr
65 70 75 80
Leu Arg Asp Gly Asn Ser Phe Ser Ala Arg Arg Val Ala Ala Ile Gln
85 90 95
Asn Gly Lys Pro Ile Phe Tyr Met Thr Ala Ser Phe Gln Ala Pro Glu
100 105 110
Ala Gly Phe Glu His Gln Lys Thr Met Pro Ser Ala Pro Ala Pro Asp
115 120 125
Gly Leu Pro Ser Glu Thr Gln Ile Ala Gln Ser Leu Ala His Leu Leu
130 135 140
Pro Pro Val Leu Lys Asp Lys Phe Ile Cys Asp Arg Pro Leu Glu Val
145 150 155 160
Arg Pro Val Glu Phe His Asn Pro Leu Lys Gly His Val Ala Glu Pro
165 170 175
His Arg Gln Val Trp Ile Arg Ala Asn Gly Ser Val Pro Asp Asp Leu
180 185 190
Arg Val His Gln Tyr Leu Leu Gly Tyr Ala Ser Asp Leu Asn Phe Leu
195 200 205
Pro Val Ala Leu Gln Pro His Gly Ile Gly Phe Leu Glu Pro Gly Ile
210 215 220
Gln Ile Ala Thr Ile Asp His Ser Met Trp Phe His Arg Pro Phe Asn
225 230 235 240
Leu Asn Glu Trp Leu Leu Tyr Ser Val Glu Ser Thr Ser Ala Ser Ser
245 250 255
Ala Arg Gly Phe Val Arg Gly Glu Phe Tyr Thr Gln Asp Gly Val Leu
260 265 270
Val Ala Ser Thr Val Gln Glu Gly Val Met Arg Asn His Asn
275 280 285

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 854594

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ala	Ser	Lys	Met	Ala	Met	Ser	Asn	Leu	Glu	Lys	Ile	Leu	Glu
1				5					10					15	
Leu	Val	Pro	Leu	Ser	Pro	Thr	Ser	Phe	Val	Thr	Lys	Tyr	Leu	Pro	Ala
			20					25					30		
Ala	Pro	Val	Gly	Ser	Lys	Gly	Thr	Phe	Gly	Gly	Thr	Leu	Val	Ser	Gln
		35				40					45				
Ser	Leu	Leu	Ala	Ser	Leu	His	Thr	Val	Pro	Leu	Asn	Phe	Phe	Pro	Thr
50					55					60					
Ser	Leu	His	Ser	Tyr	Phe	Ile	Lys	Gly	Gly	Asp	Pro	Arg	Thr	Lys	Ile
65				70					75					80	
Thr	Tyr	His	Val	Gln	Asn	Leu	Arg	Asn	Gly	Arg	Asn	Phe	Ile	His	Lys
			85					90					95		
Gln	Val	Ser	Ala	Tyr	Gln	His	Asp	Lys	Leu	Ile	Phe	Thr	Ser	Met	Ile
			100					105					110		
Leu	Phe	Ala	Val	Gln	Arg	Ser	Lys	Glu	His	Asp	Ser	Leu	Gln	His	Trp
		115					120					125			
Glu	Thr	Ile	Pro	Gly	Leu	Gln	Gly	Lys	Gln	Pro	Asp	Pro	His	Arg	Tyr
130					135					140					
Glu	Glu	Ala	Thr	Ser	Leu	Phe	Gln	Lys	Glu	Val	Leu	Asp	Pro	Gln	Lys
145					150					155				160	
Leu	Ser	Arg	Tyr	Ala	Ser	Leu	Ser	Asp	Arg	Phe	Gln	Asp	Ala	Thr	Ser
			165					170						175	
Met	Ser	Lys	Tyr	Val	Asp	Ala	Phe	Gln	Tyr	Gly	Val	Met	Glu	Tyr	Gln
			180					185					190		
Phe	Pro	Lys	Asp	Met	Phe	Tyr	Ser	Ala	Arg	His	Thr	Asp	Glu	Leu	Asp
		195					200					205			
Tyr	Phe	Val	Lys	Val	Arg	Pro	Pro	Ile	Thr	Thr	Val	Glu	His	Ala	Gly
210						215					220				
Asp	Glu	Ser	Ser	Leu	His	Lys	His	His	Pro	Tyr	Arg	Ile	Pro	Lys	Ser
225				230						235				240	
Ile	Thr	Pro	Glu	Asn	Asp	Ala	Arg	Tyr	Asn	Tyr	Val	Ala	Phe	Ala	Tyr
			245					250					255		
Leu	Ser	Asp	Ser	Tyr	Leu	Leu	Leu	Thr	Ile	Pro	Tyr	Phe	His	Asn	Leu
			260					265					270		
Pro	Leu	Tyr	Cys	His	Ser	Phe	Ser	Val	Ser	Leu	Asp	His	Thr	Ile	Tyr
		275					280					285			
Phe	His	Gln	Leu	Pro	His	Val	Asn	Asn	Trp	Ile	Tyr	Leu	Lys	Ile	Ser
		290				295					300				
Asn	Pro	Arg	Ser	His	Trp	Asp	Lys	His	Leu	Val	Gln	Gly	Lys	Tyr	Phe
305					310					315				320	
Asp	Thr	Gln	Ser	Gly	Arg	Ile	Met	Ala	Ser	Val	Ser	Gln	Glu	Gly	Tyr
			325					330					335		
Val	Val	Tyr	Gly	Ser	Glu	Arg	Asp	Ile	Arg	Ala	Lys	Phe			
			340					345							

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